

COPY

PCTUS2004037793.seq.list.txt
SEQUENCE LISTING

<110> UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.

<120> DNA SEQUENCE AND EXPRESSED RECOMBINANT GLYCOPROTEINS
RELATED TO FELINE THYROTROPIN

<130> 235-00540201

<140> PCT/US04/03779

<141> 2004-11-12

<150> 60/534,205

<151> 2004-01-05

<150> 60/519,302

<151> 2003-11-12

<160> 18

<170> PatentIn Ver. 3.3

<210> 1

<211> 118

<212> PRT

<213> Felis sp.

<400> 1

Phe Cys Phe Pro Thr Glu Tyr Met Met His Val Glu Arg Lys Glu Cys
1 5 10 15

Ala Tyr Cys Leu Thr Ile Asn Thr Thr Ile Cys Ala Gly Tyr Cys Met
20 25 30

Thr Arg Asp Ile Asn Gly Lys Leu Phe Leu Pro Lys Tyr Ala Leu Ser
35 40 45

Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys Thr Val Glu Ile
50 55 60

Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser Tyr Pro Val Ala
65 70 75 80

Val Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr Ser Asp Cys Ile
85 90 95

His Glu Ala Ile Lys Thr Asn Asp Cys Thr Lys Pro Gln Lys Ser Asp
100 105 110

Val Val Gly Val Ser Ile
115

<210> 2

<211> 138

<212> PRT

<213> Felis sp.

<400> 2

Met Thr Ala Ile Tyr Leu Met Ser Val Leu Phe Gly Leu Ala Cys Gly
1 5 10 15

Gln Ala Met Ser Phe Cys Phe Pro Thr Glu Tyr Met Met His Val Glu
Page 1

PCTUS2004037793.seq.list.txt

Arg Lys Glu²⁰ Cys³⁵ Ala Tyr Cys⁴⁰ Leu²⁵ Thr⁴⁵ Ile Asn Thr³⁰ Thr⁴⁵ Ile Cys Ala
 Gly Tyr Cys Met Thr Arg Asp⁵⁵ Ile Asn Gly Lys⁶⁰ Leu Phe Leu Pro Lys
 Tyr Ala Leu Ser Gln⁷⁰ Asp⁷⁵ Val Cys Thr Tyr Arg⁷⁵ Asp Phe Leu Tyr Lys⁸⁰
 Thr Val Glu Ile⁸⁵ Pro Gly Cys Pro His His⁹⁰ Val Thr Pro Tyr Phe⁹⁵ Ser
 Tyr Pro Val¹⁰⁰ Ala Val Ser Cys Lys¹⁰⁵ Gly Lys Cys Asn¹¹⁰ Thr Asp Tyr
 Ser Asp Cys¹¹⁵ Ile His Glu Ala Ile¹²⁰ Lys Thr Asn Asp Cys¹²⁵ Thr Lys Pro
 Gln Lys Ser Asp Val Val¹³⁰ Gly¹³⁵ Val Ser Ile

<210> 3
 <211> 96
 <212> PRT
 <213> Felis sp.

<400> 3
 Phe Pro Asp Gly Glu⁵ Phe Thr Met Gln Gly¹⁰ Cys Pro Glu Cys Lys¹⁵ Leu
 Lys Glu Asn Lys²⁰ Tyr Phe Ser Lys²⁵ Leu Gly Ala Pro Ile Tyr³⁰ Gln Cys
 Met Gly Cys³⁵ Cys Phe Ser Arg Ala Tyr Pro Thr Pro Ala⁴⁵ Arg Ser Lys
 Lys Thr Met Leu Val Pro Lys⁵⁵ Asn Ile Thr Ser Glu⁶⁰ Ala Thr Cys Cys
 Val Ala Lys Ala Phe Thr⁷⁰ Lys Ala Thr Val Met⁷⁵ Gly Asn Ala Lys Val⁸⁰
 Glu Asn His Thr⁸⁵ Glu Cys His Cys Ser Thr⁹⁰ Cys Tyr His His Lys⁹⁵ Ile

<210> 4
 <211> 120
 <212> PRT
 <213> Felis sp.

<400> 4
 Met Asp Tyr Tyr Arg⁵ Lys Tyr Ala Ala Val¹⁰ Ile Leu Ala Ile Lys¹⁵ Ser
 Val Phe Leu His²⁰ Ile Leu His Ser Phe²⁵ Pro Asp Gly Glu Phe Thr Met
 Gln Gly Cys³⁵ Pro Glu Cys Lys Leu⁴⁰ Lys Glu Asn Lys Tyr⁴⁵ Phe Ser Lys

PCTUS2004037793.seq.list.txt

Leu Gly Ala Pro Ile Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala
 50 55 60
 Tyr Pro Thr Pro Ala Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn
 65 70 75 80
 Ile Thr Ser Glu Ala Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala
 85 90 95
 Thr Val Met Gly Asn Ala Lys Val Glu Asn His Thr Glu Cys His Cys
 100 105 110
 Ser Thr Cys Tyr His His Lys Ile
 115 120

<210> 5
 <211> 244
 <212> PRT
 <213> Felis sp.

<400> 5
 Phe Cys Phe Pro Thr Glu Tyr Met Met His Val Glu Arg Lys Glu Cys
 1 5 10 15
 Ala Tyr Cys Leu Thr Ile Asn Thr Thr Ile Cys Ala Gly Tyr Cys Met
 20 25 30
 Thr Arg Asp Ile Asn Gly Lys Leu Phe Leu Pro Lys Tyr Ala Leu Ser
 35 40 45
 Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys Thr Val Glu Ile
 50 55 60
 Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser Tyr Pro Val Ala
 65 70 75 80
 Val Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr Ser Asp Cys Ile
 85 90 95
 His Glu Ala Ile Lys Thr Asn Asp Cys Thr Lys Pro Gln Lys Ser Asp
 100 105 110
 Val Val Gly Val Ser Ile Gln Asp Ser Ser Ser Ser Lys Ala Pro Ser
 115 120 125
 Ala Ser Leu Pro Ser Pro Thr Arg Leu Pro Gly Pro Ser Asp Thr Pro
 130 135 140
 Ile Leu Pro Gln Phe Pro Asp Gly Glu Phe Thr Met Gln Gly Cys Pro
 145 150 155 160
 Glu Cys Lys Leu Lys Glu Asn Lys Tyr Phe Ser Lys Leu Gly Ala Pro
 165 170 175
 Ile Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro
 180 185 190
 Ala Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn Ile Thr Ser Glu
 195 200 205
 Ala Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala Thr Val Met Gly
 210 215 220

Asn Ala Lys Val Glu Asn His Thr Glu Cys His Cys Ser Thr Cys Tyr
 225 230 235 240

His His Lys Ile

<210> 6

<211> 264

<212> PRT

<213> Felis sp.

<400> 6

Met Thr Ala Ile Tyr Leu Met Ser Val Leu Phe Gly Leu Ala Cys Gly
 1 5 10 15

Gln Ala Met Ser Phe Cys Phe Pro Thr Glu Tyr Met Met His Val Glu
 20 25 30

Arg Lys Glu Cys Ala Tyr Cys Leu Thr Ile Asn Thr Thr Ile Cys Ala
 35 40 45

Gly Tyr Cys Met Thr Arg Asp Ile Asn Gly Lys Leu Phe Leu Pro Lys
 50 55 60

Tyr Ala Leu Ser Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys
 65 70 75 80

Thr Val Glu Ile Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser
 85 90 95

Tyr Pro Val Ala Val Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr
 100 105 110

Ser Asp Cys Ile His Glu Ala Ile Lys Thr Asn Asp Cys Thr Lys Pro
 115 120 125

Gln Lys Ser Asp Val Val Gly Val Ser Ile Gln Asp Ser Ser Ser Ser
 130 135 140

Lys Ala Pro Ser Ala Ser Leu Pro Ser Pro Thr Arg Leu Pro Gly Pro
 145 150 155 160

Ser Asp Thr Pro Ile Leu Pro Gln Phe Pro Asp Gly Glu Phe Thr Met
 165 170 175

Gln Gly Cys Pro Glu Cys Lys Leu Lys Glu Asn Lys Tyr Phe Ser Lys
 180 185 190

Leu Gly Ala Pro Ile Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala
 195 200 205

Tyr Pro Thr Pro Ala Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn
 210 215 220

Ile Thr Ser Glu Ala Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala
 225 230 235 240

Thr Val Met Gly Asn Ala Lys Val Glu Asn His Thr Glu Cys His Cys
 245 250 255

Ser Thr Cys Tyr His His Lys Ile
 260

PCTUS2004037793.seq.list.txt

<210> 7
 <211> 417
 <212> DNA
 <213> Felis sp.

<220>
 <221> CDS
 <222> (1)..(414)
 <223> coding region for SEQ ID NO: 2

<220>
 <221> CDS
 <222> (61)..(414)
 <223> coding region for SEQ ID NO: 1

```

<400> 7
atg act gct atc tac ctg atg tcc gtg ctt ttt ggc ctg gca tgt gga 48
Met Thr Ala Ile Tyr Leu Met Ser Val Leu Phe Gly Leu Ala Cys Gly
      1              5              10              15

caa gcg atg tct ttt tgt ttt cca act gag tat atg atg cat gtc gaa 96
Gln Ala Met Ser Phe Cys Phe Pro Thr Glu Tyr Met Met His Val Glu
              20              25              30

agg aaa gag tgt gct tat tgc cta acc atc aac acc acc atc tgt gct 144
Arg Lys Glu Cys Ala Tyr Cys Leu Thr Ile Asn Thr Thr Ile Cys Ala
              35              40              45

gga tat tgt atg aca cgg gat atc aat ggc aaa ctg ttt ctt ccc aaa 192
Gly Tyr Cys Met Thr Arg Asp Ile Asn Gly Lys Leu Phe Leu Pro Lys
      50              55              60

tat gct ctg tcc caa gat gtt tgc acc tac aga gac ttc ctg tac aag 240
Tyr Ala Leu Ser Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys
      65              70              75              80

act gta gaa ata cca gga tgc cca cac cat gtt act ccc tat ttc tcc 288
Thr Val Glu Ile Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser
              85              90              95

tac ccg gta gct gta agc tgt aaa tgt ggc aag tgt aat act gac tat 336
Tyr Pro Val Ala Val Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr
              100              105              110

agc gac tgc ata cat gag gcc atc aag aca aat gat tgt acc aaa ccc 384
Ser Asp Cys Ile His Glu Ala Ile Lys Thr Asn Asp Cys Thr Lys Pro
      115              120              125

cag aag tcc gat gtg gta gga gtt tct atc taa 417
Gln Lys Ser Asp Val Val Gly Val Ser Ile
      130              135
    
```

<210> 8
 <211> 835
 <212> DNA
 <213> Felis sp.

```

<400> 8
atgactgcta tctacctgat gtccgtgctt tttggcctgg catgtggaca agcgatgtct 60
ttttgttttc caactgagta tatgatgcat gtcgaaagga aagagtgtgc ttattgccta 120
accatcaaca ccaccatctg tgctggatat tgtatgacac gggtatgtag ttcattcac 180
    
```

PCTUS2004037793.seq.list.txt

```

ttcttttagc tgaaaattag ataaacctag actcagtcga tttctatcca gaaaggaaat 240
gagataaatc acaacctcat ttccagagacc taacgggtcat tggctcctta gaggtagagt 300
ccctaggtta taatatatcg acctactcca tacagttggg acagataatt ttacaatag 360
ttttactccc aaagtttatt taaaccttat cttgttccca cgatcaagga taaaagagag 420
gtgtgtgtgt atgtcatttt tttttgtctc tataggattc agtgtggata tgctgaattg 480
gtattgggga atgggactaa ggaatcctcc cccagtccta tttgtatcta tgggatgtaa 540
gcgaattaac attttgcttc ctcttctgtg cttccctcag gatatacatg gcaaaactgtt 600
tcttcccaaa tatgtctctgt cccaagatgt ttgcacctac agagacttcc tgtacaagac 660
tgtagaaata ccaggatgcc cacaccatgt tactccctat ttctcctacc cggtagctgt 720
aagctgtaaa tgtggcaagt gtaatactga ctatagcgac tgcatacatg aggccatcaa 780
gacaaatgat tgtaccaaac cccagaagtc cgatgtggta ggagtttcta tctaa 835

```

<210> 9
 <211> 360
 <212> DNA
 <213> Felis sp.

```

<400> 9
atggattact acagaaaata tgcagctgtc attctggcca tactctctgt gtttctgcat 60
attctccatt cttttcctga tggagagttt acaatgcagg ggtgcccaga atgcaagcta 120
aaggaaaaca aatacttctc caagttgggt gcccacaatt atcaatgcat gggctgctgc 180
ttctccagag catacccccac tccagcaagg tccaagaaga caatgttggg cccaaagaac 240
atcacctcag aagccacatg ctgtgtggcc aaagccttta ccaaggccac ggtaatggga 300
aatgccaag tggagaatca cacagagtgc cactgcagca cttgctatca ccacaagatt 360

```

<210> 10
 <211> 459
 <212> DNA
 <213> Felis sp.

<220>
 <221> CDS
 <222> (100)..(459)
 <223> coding region for SEQ ID NO: 4

<220>
 <221> CDS
 <222> (172)..(459)
 <223> coding region for SEQ ID NO: 3

```

<400> 10
agttactgag aaatcacaag acgaagccaa aatccctctt cagatccacg gtcaactgcc 60

ctgatcacat cctgcaaaaa gtccggagga aggagagccc atg gat tac tac aga 114
                                     Met Asp Tyr Tyr Arg
                                     1 5

aaa tat gca gct gtc att ctg gcc ata ctc tct gtg ttt ctg cat att 162
Lys Tyr Ala Ala Val Ile Leu Ala Ile Leu Ser Val Phe Leu His Ile
                                     10 15 20

ctc cat tct ttt cct gat gga gag ttt aca atg cag ggg tgc cca gaa 210
Leu His Ser Phe Pro Asp Gly Glu Phe Thr Met Gln Gly Cys Pro Glu
                                     25 30 35

tgc aag cta aag gaa aac aaa tac ttc tcc aag ttg ggt gcc cca att 258
Cys Lys Leu Lys Glu Asn Lys Tyr Phe Ser Lys Leu Gly Ala Pro Ile
                                     40 45 50

tat caa tgc atg ggc tgc tgc ttc tcc aga gca tac ccc act cca gca 306
Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Ala

```

55	60		
agg tcc aag aag aca atg ttg gtc cca aag aac atc acc tca gaa gcc	354		
Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn Ile Thr Ser Glu Ala			
70 75 80 85			
aca tgc tgt gtg gcc aaa gcc ttt acc aag gcc acg gta atg gga aat	402		
Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala Thr Val Met Gly Asn			
90 95 100			
gcc aaa gtg gag aat cac aca gag tgc cac tgc agc act tgc tat cac	450		
Ala Lys Val Glu Asn His Thr Glu Cys His Cys Ser Thr Cys Tyr His			
105 110 115			
cac aag att	459		
His Lys Ile			
120			
<210> 11			
<211> 792			
<212> DNA			
<213> Felis sp.			
<220>			
<221> CDS			
<222> (1)..(792)			
<223> coding region for SEQ ID NO: 6			
<220>			
<221> CDS			
<222> (61)..(792)			
<223> coding region for SEQ ID NO: 5			
<400> 11			
atg act gct atc tac ctg atg tcc gtg ctt ttt ggc ctg gca tgt gga	48		
Met Thr Ala Ile Tyr Leu Met Ser Val Leu Phe Gly Leu Ala Cys Gly			
1 5 10 15			
caa gcg atg tct ttt tgt ttt cca act gag tat atg atg cat gtc gaa	96		
Gln Ala Met Ser Phe Cys Phe Pro Thr Glu Tyr Met Met His Val Glu			
20 25 30			
agg aaa gag tgt gct tat tgc cta acc atc aac acc acc atc tgt gct	144		
Arg Lys Glu Cys Ala Tyr Cys Leu Thr Ile Asn Thr Thr Ile Cys Ala			
35 40 45			
gga tat tgt atg aca cgg gat atc aat ggc aaa ctg ttt ctt ccc aaa	192		
Gly Tyr Cys Met Thr Arg Asp Ile Asn Gly Lys Leu Phe Leu Pro Lys			
50 55 60			
tat gct ctg tcc caa gat gtt tgc acc tac aga gac ttc ctg tac aag	240		
Tyr Ala Leu Ser Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys			
65 70 75 80			
act gta gaa ata cca gga tgc cca cac cat gtt act ccc tat ttc tcc	288		
Thr Val Glu Ile Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser			
85 90 95			
tac ccg gta gct gta agc tgt aaa tgt ggc aag tgt aat act gac tat	336		
Tyr Pro Val Ala Val Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr			
100 105 110			

PCTUS2004037793.seq.list.txt

agc gac tgc ata cat gag gcc atc aag aca aat gat tgt acc aaa ccc	384
Ser Asp Cys Ile His Glu Ala Ile Lys Thr Asn Asp Cys Thr Lys Pro	
115 120 125	
cag aag tcc gat gtg gta gga gtt tct atc cag gac tcc tct tcc tca	432
Gln Lys Ser Asp Val Val Gly Val Ser Ile Gln Asp Ser Ser Ser Ser	
130 135 140	
aag gcc cct tcc gcc agc ctt cca agc cca acg cgt ctc ccg ggg ccc	480
Lys Ala Pro Ser Ala Ser Leu Pro Ser Pro Thr Arg Leu Pro Gly Pro	
145 150 155 160	
tcg gac acc ccg atc ctc cca caa ttt cct gat gga gag ttt aca atg	528
Ser Asp Thr Pro Ile Leu Pro Gln Phe Pro Asp Gly Glu Phe Thr Met	
165 170 175	
cag ggg tgc cca gaa tgc aag cta aag gaa aac aaa tac ttc tcc aag	576
Gln Gly Cys Pro Glu Cys Lys Leu Lys Glu Asn Lys Tyr Phe Ser Lys	
180 185 190	
ttg ggt gcc cca att tat caa tgc atg ggc tgc tgc ttc tcc aga gca	624
Leu Gly Ala Pro Ile Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala	
195 200 205	
tac ccc act cca gca agg tcc aag aag aca atg ttg gtc cca aag aac	672
Tyr Pro Thr Pro Ala Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn	
210 215 220	
atc acc tca gaa gcc aca tgc tgt gtg gcc aaa gcc ttt acc aag gcc	720
Ile Thr Ser Glu Ala Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala	
225 230 235 240	
acg gta atg gga aat gcc aaa gtg gag aat cac aca gag tgc cac tgc	768
Thr Val Met Gly Asn Ala Lys Val Glu Asn His Thr Glu Cys His Cys	
245 250 255	
agc act tgc tat cac cac aag att	792
Ser Thr Cys Tyr His His Lys Ile	
260	

<210> 12
 <211> 1210
 <212> DNA
 <213> Felis sp.

<400> 12

atgactgcta	tctacctgat	gtccgtgctt	tttggcctgg	catgtggaca	agcgatgtct	60
ttttgttttc	caactgagta	tatgatgcat	gtcgaagga	aagagtgtgc	ttattgccta	120
accatcaaca	ccaccatctg	tgtctggatat	tgtatgacac	gggtatgtag	ttcatctcac	180
ttcttttagc	tgaaaattag	ataaacctag	actcagtcca	tttctatcca	gaaaggaaat	240
gagataaatc	acaacctcat	ttcacagacc	taacggtcat	tggctcctta	gaggtagagt	300
ccctaggtta	taatatacgg	acctactcca	tacagttagt	acagataatt	tttacaatag	360
ttttactccc	aaagtttatt	taaacccttat	cttgttccca	cgatcaagga	taaaagagag	420
gtgtgtgtgt	atgtcatttt	tttttgtctc	tataggattc	agtgtggata	tgctgaattg	480
gtattgggga	atgggactaa	ggaatcctcc	cccagtccta	tttgtatcta	tgggatgtaa	540
gcgaattaac	attttgcttc	ctcttctgtg	cttccctcag	gatataaatg	gcaaactggt	600
tcttcccaaa	tatgctctgt	cccaagatgt	ttgcacctac	agagacttcc	tgtacaagac	660
tgtagaataa	ccaggatgcc	cacaccatgt	tactccctat	ttctcctacc	cggtagctgt	720
aagctgtaaa	tgtggcaagt	gtaatactga	ctatagcgac	tgcatacatg	aggccatcaa	780
gacaaatgat	tgtaccaaac	cccagaagtc	cgatgtggta	ggagtgttcta	tccaggactc	840
ctcttctca	aaggccctt	ccgccagcct	tccaagccca	acgcgtctcc	cggggccctc	900
ggacaccccg	atcctccac	aatttcctga	tggagagttt	acaatgcagg	ggtgcccaga	960
atgcaagcta	aaggaaaaca	aatacttctc	caagttaggt	gccccaat	atcaatgcat	1020

PCTUS2004037793.seq.list.txt

```

gggctgctgc ttctccagag catacccccac tccagcaagg tccaagaaga caatgttggt 1080
cccaaagaac atcacctcag aagccacatg ctgtgtggcc aaagccttta ccaaggccac 1140
ggtaatggga aatgccaaag tggagaatca cacagagtgc cactgcagca cttgctatca 1200
ccacaagatt                                     1210

```

<210> 13
 <211> 130
 <212> DNA
 <213> Felis sp.

```

<400> 13
gtccgatgtg gtaggagttt ctatccagga ctctctttcc tcaaaggccc cttccgccag 60
ccttccaagc ccaacgcgtc tcccggggcc ctcggaacac ccgatcctcc cacaatttcc 120
tgatggagag                                     130

```

<210> 14
 <211> 851
 <212> DNA
 <213> Felis sp.

```

<400> 14
gaattcatga ctgctatcta cctgatgtcc gtgctttttg gcctggcatg tggacaagcg 60
atgtcttttt gttttccaac tgagtatatg atgcatgtcg aaaggaaaga gtgtgcttat 120
tgcctaacca tcaacaccac catctgtgct ggatattgta tgacacgggt atgtagttca 180
tctcacttct tttagctgaa aattagataa acctagactc agtccatttc tatccagaaa 240
ggaaatgaga taaatcacia cctcatttca cagacctaac ggtcattggc tccttagagg 300
tagagtccct aggttataat atacggacct actccataca gttggtacag ataattttta 360
caatagtttt actcccaaag tttattttaa cttatcttgg tttccacgat caaggataaa 420
agagaggtgt gtgtgtatgt cttttttttt tgtctctata ggattcagtg tggatatgct 480
gaattgggat tggggaatgg gactaaggaa tcctcccca gtcctatttg tatctatggg 540
atgtaagcga attaacattt tgcttctctt tctgtgcttc cctcaggata tcaatggcaa 600
actgtttctt cccaaatatg ctctgtccca agatgtttgc acctacagag acttccctga 660
caagactgtg gaaataccag gatgccaca ccattgttact ccctatttct cctaccgggt 720
agctgtaagc tgtaaatgtg gcaagtgtaa tactgactat agcgactgca tacatgaggc 780
catcaagaca aatgattgta ccaaaccaca gaagtccgat gtggtaggag tttctatcta 840
agcggccgca t                                     851

```

<210> 15
 <211> 522
 <212> DNA
 <213> Felis sp.

<220>
 <221> CDS
 <222> (112)..(507)

```

<400> 15
gaattcgccc ttagttactg agaaatcaca agacgaagcc aaaatccctc ttcagatcca 60

```

```

cgggtcaactg ccctgatcac atcctgcaaa aagtccggag gaaggagagc c atg gat 117
                                     Met Asp
                                     1

```

```

tac tac aga aaa tat gca gct gtc att ctg gcc ata ctc tct gtg ttt 165
Tyr Tyr Arg Lys Tyr Ala Ala Val Ile Leu Ala Ile Leu Ser Val Phe
          5                10                15

```

```

ctg cat att ctc cat tct ttt cct gat gga gag ttt aca atg cag ggg 213
Leu His Ile Leu His Ser Phe Pro Asp Gly Glu Phe Thr Met Gln Gly
    20                25                30

```

PCTUS2004037793.seq.list.txt

tgc cca gaa tgc aag cta aag gaa aac aaa tac ttc tcc aag ttg ggt	261
Cys Pro Glu Cys Lys Leu Lys Glu Asn Lys Tyr Phe Ser Lys Leu Gly	
35 40 45 50	
gcc cca att tat caa tgc atg ggc tgc tgc ttc tcc aga gca tac ccc	309
Ala Pro Ile Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro	
55 60 65	
act cca gca agg tcc aag aag aca atg ttg gtc cca aag aac atc acc	357
Thr Pro Ala Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn Ile Thr	
70 75 80	
tca gaa gcc aca tgc tgt gtg gcc aaa gcc ttt acc aag gcc acg gta	405
Ser Glu Ala Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala Thr Val	
85 90 95	
atg gga aat gcc aaa gtg gag aat cac aca gag tgc cac tgc agc act	453
Met Gly Asn Ala Lys Val Glu Asn His Thr Glu Cys His Cys Ser Thr	
100 105 110	
tgc tat cac cac aag att atc gaa ggt cgt gac tac aag gac gat gac	501
Cys Tyr His His Lys Ile Ile Glu Gly Arg Asp Tyr Lys Asp Asp Asp	
115 120 125 130	
gat aag taagcggccg ctatg	522
Asp Lys	

<210> 16
 <211> 132
 <212> PRT
 <213> Felis sp.

<400> 16
 Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Val Ile Leu Ala Ile Leu Ser
 1 5 10 15
 Val Phe Leu His Ile Leu His Ser Phe Pro Asp Gly Glu Phe Thr Met
 20 25 30
 Gln Gly Cys Pro Glu Cys Lys Leu Lys Glu Asn Lys Tyr Phe Ser Lys
 35 40 45
 Leu Gly Ala Pro Ile Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala
 50 55 60
 Tyr Pro Thr Pro Ala Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn
 65 70 75 80
 Ile Thr Ser Glu Ala Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala
 85 90 95
 Thr Val Met Gly Asn Ala Lys Val Glu Asn His Thr Glu Cys His Cys
 100 105 110
 Ser Thr Cys Tyr His His Lys Ile Ile Glu Gly Arg Asp Tyr Lys Asp
 115 120 125
 Asp Asp Asp Lys
 130

```
<210> 17
<211> 1267
<212> DNA
<213> Felis sp.
```

```
<220>  
<221> CDS  
<222> (587)..(1252)
```

aaa ccc cag aag tcc gat gtg qta gga qtt tct atc cag qac tcc tct 850

PCTUS2004037793.seq.list.txt

Lys	Pro	Gln	Lys	Ser	Asp	Val	Val	Gly	Val	Ser	Ile	Gln	Asp	Ser	Ser		
			130					135					140				
tcc	tca	aag	gcc	cct	tcc	gcc	agc	ctt	cca	agc	cca	acg	cg	ctc	ccg		898
Ser	Ser	Lys	Ala	Pro	Ser	Ala	Ser	Leu	Pro	Ser	Pro	Thr	Arg	Leu	Pro		
		145					150					155					
ggg	ccc	tcg	gac	acc	ccg	atc	ctc	cca	caa	ttt	cct	gat	gga	gag	ttt		946
Gly	Pro	Ser	Asp	Thr	Pro	Ile	Leu	Pro	Gln	Phe	Pro	Asp	Gly	Glu	Phe		
	160					165					170						
aca	atg	cag	ggg	tgc	cca	gaa	tgc	aag	cta	aag	gaa	aac	aaa	tac	ttc		994
Thr	Met	Gln	Gly	Cys	Pro	Glu	Cys	Lys	Leu	Lys	Glu	Asn	Lys	Tyr	Phe		
175					180			185							190		
tcc	aag	ttg	ggt	gcc	cca	att	tat	caa	tgc	atg	ggc	tgc	tgc	ttc	tcc		1042
Ser	Lys	Leu	Gly	Ala	Pro	Ile	Tyr	Gln	Cys	Met	Gly	Cys	Cys	Phe	Ser		
				195				200						205			
aga	gca	tac	ccc	act	cca	gca	agg	tcc	aag	aag	aca	atg	ttg	gtc	cca		1090
Arg	Ala	Tyr	Pro	Thr	Pro	Ala	Arg	Ser	Lys	Lys	Thr	Met	Leu	Val	Pro		
			210					215					220				
aag	aac	atc	acc	tca	gaa	gcc	aca	tgc	tgt	gtg	gcc	aaa	gcc	ttt	acc		1138
Lys	Asn	Ile	Thr	Ser	Glu	Ala	Thr	Cys	Cys	Val	Ala	Lys	Ala	Phe	Thr		
		225					230					235					
aag	gcc	acg	gta	atg	gga	aat	gcc	aaa	gtg	gag	aat	cac	aca	gag	tgc		1186
Lys	Ala	Thr	Val	Met	Gly	Asn	Ala	Lys	Val	Glu	Asn	His	Thr	Glu	Cys		
	240				245						250						
cac	tgc	agc	act	tgc	tat	cac	cac	aag	att	atc	gaa	ggc	cg	gac	tac		1234
His	Cys	Ser	Thr	Cys	Tyr	His	His	Lys	Ile	Ile	Glu	Gly	Arg	Asp	Tyr		
255				260					265						270		
aag	gac	gat	gac	gat	aag	taagcggccg ctatg											1267
Lys	Asp	Asp	Asp	Asp	Lys												
				275													

<210> 18
 <211> 276
 <212> PRT
 <213> Felis sp.

<400> 18
 Met Thr Ala Ile Tyr Leu Met Ser Val Leu Phe Gly Leu Ala Cys Gly
 1 5 10 15
 Gln Ala Met Ser Phe Cys Phe Pro Thr Glu Tyr Met Met His Val Glu
 20 25 30
 Arg Lys Glu Cys Ala Tyr Cys Leu Thr Ile Asn Thr Thr Ile Cys Ala
 35 40 45
 Gly Tyr Cys Met Thr Arg Asp Ile Asn Gly Lys Leu Phe Leu Pro Lys
 50 55 60
 Tyr Ala Leu Ser Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys
 65 70 75 80
 Thr Val Glu Ile Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser
 85 90 95

PCTUS2004037793.seq.list.txt

Tyr	Pro	Val	Ala	Val	Ser	Cys	Lys	Cys	Gly	Lys	Cys	Asn	Thr	Asp	Tyr
			100					105					110		
Ser	Asp	Cys	Ile	His	Glu	Ala	Ile	Lys	Thr	Asn	Asp	Cys	Thr	Lys	Pro
		115					120					125			
Gln	Lys	Ser	Asp	Val	Val	Gly	Val	Ser	Ile	Gln	Asp	Ser	Ser	Ser	Ser
	130					135					140				
Lys	Ala	Pro	Ser	Ala	Ser	Leu	Pro	Ser	Pro	Thr	Arg	Leu	Pro	Gly	Pro
145					150					155					160
Ser	Asp	Thr	Pro	Ile	Leu	Pro	Gln	Phe	Pro	Asp	Gly	Glu	Phe	Thr	Met
				165					170					175	
Gln	Gly	Cys	Pro	Glu	Cys	Lys	Leu	Lys	Glu	Asn	Lys	Tyr	Phe	Ser	Lys
			180					185					190		
Leu	Gly	Ala	Pro	Ile	Tyr	Gln	Cys	Met	Gly	Cys	Cys	Phe	Ser	Arg	Ala
		195					200					205			
Tyr	Pro	Thr	Pro	Ala	Arg	Ser	Lys	Lys	Thr	Met	Leu	Val	Pro	Lys	Asn
	210					215					220				
Ile	Thr	Ser	Glu	Ala	Thr	Cys	Cys	Val	Ala	Lys	Ala	Phe	Thr	Lys	Ala
225					230					235					240
Thr	Val	Met	Gly	Asn	Ala	Lys	Val	Glu	Asn	His	Thr	Glu	Cys	His	Cys
				245					250					255	
Ser	Thr	Cys	Tyr	His	His	Lys	Ile	Ile	Glu	Gly	Arg	Asp	Tyr	Lys	Asp
			260					265					270		
Asp	Asp	Asp	Lys												
		275													